

SEQUENCE LISTING

<110> Croteau, Rodney et al.

<120> Transacylases of the Paclitaxel Biosynthetic Pathway

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<150> 09/411,145

<151> 1999-09-30

<160> 58

<170> PatentIn Ver. 2.0

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<212> DNA

<213> Taxus cuspidata

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<213> Taxus cuspidata

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Glu Ala Met Ala Asp Asn Glu Leu Ser Val Leu Gly Asp Phe Asp Asp
      35                      40                      45

Ser Asn Pro Ser Phe Gln Gln Leu Leu Phe Ser Leu Pro Leu Asp Thr
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Asn Phe Lys Asp Leu Ser Leu Leu Val Val Gln Val Thr Arg Phe Thr
      65                      70                      75                      80

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 Lys Leu Asp Asp Pro Lys Tyr Leu Gln Phe Phe His Phe Glu Phe Leu
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 Arg Ala Pro Ser Ile Val Glu Lys Ile Val Gln Thr Tyr Phe Ile Ile
 145 150 155 160
 Asp Leu Glu Thr Ile Asn Tyr Ile Lys Gln Ser Val Met Glu Glu Cys
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 Lys Glu Phe Cys Ser Ser Phe Glu Val Ala Ser Ala Met Thr Trp Ile
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 Ala Arg Thr Arg Ala Phe Gln Ile Pro Glu Ser Glu Tyr Val Lys Ile
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 Gly Tyr Tyr Gly Asn Ser Ile Gly Thr Ala Cys Ala Val Asp Asn Val
 225 230 235 240
 Gln Asp Leu Leu Ser Gly Ser Leu Leu Arg Ala Ile Met Ile Ile Lys
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 Lys Ser Lys Val Ser Leu Asn Asp Asn Phe Lys Ser Arg Ala Val Val
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      20             25             30

Glu Ala Met Ala Asp Asn Asp Leu Ser Val Leu Gln Asp Phe Asn Glu
      35             40             45

Tyr Asp Pro Ser Phe Gln Gln Leu Val Phe Tyr Leu Pro Glu Asp Val
      50             55             60

Asn Ile Glu Asp Leu His Leu Leu Thr Val Gln Val Thr Arg Phe Thr
      65             70             75             80

Cys Gly Gly Phe Val Val Gly Thr Arg Phe His His Ser Val Ser Asp
      85             90             95

Gly Lys Gly Ile Gly Gln Leu Leu Lys Gly Met Gly Glu Met Ala Arg
      100            105            110

Gly Glu Phe Lys Pro Ser Leu Glu Pro Ile Trp Asn Arg Glu Met Val
      115            120            125

Lys Pro Glu Asp Ile Met Tyr Leu Gln Phe Asp His Phe Asp Phe Ile
      130            135            140

His Pro Pro Leu Asn Leu Glu Lys Ser Ile Gln Ala Ser Met Val Ile
      145            150            155            160

Ser Leu Glu Arg Ile Asn Tyr Ile Lys Arg Cys Met Met Glu Glu Cys
      165            170            175

Lys Glu Phe Phe Ser Ala Phe Glu Val Val Val Ala Leu Ile Trp Leu
      180            185            190

Ala Arg Thr Lys Ser Phe Arg Ile Pro Pro Asn Glu Tyr Val Lys Ile
      195            200            205

Ile Phe Pro Ile Asp Met Arg Asn Ser Phe Asp Ser Pro Leu Pro Lys
      210            215            220

Gly Tyr Tyr Gly Asn Ala Ile Gly Asn Ala Cys Ala Met Asp Asn Val
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Lys Asp Leu Leu Asn Gly Ser Leu Leu Tyr Ala Leu Met Leu Ile Lys

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245

250

255

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Lys Pro Ser Ala Leu Asp Ala Asn Met Lys His Glu Asn Val Val Gly
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<213> *Taxus cuspidata*

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Asp Ser Asp Leu Ser Val Leu Thr Asp Leu Asp Asp Tyr Lys Pro Ser
35          40          45

Phe Gln Gln Leu Ile Phe Ser Leu Pro Gln Asp Thr Asp Ile Glu Asp
50          55          60

Leu His Leu Leu Ile Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe
65          70          75          80

Val Val Gly Ala Asn Val Tyr Ser Ser Val Cys Asp Ala Lys Gly Phe
85          90          95

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Gly Gln Phe Leu Gln Gly Met Ala Glu Met Ala Arg Gly Glu Val Lys
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 Pro Ser Ile Glu Pro Ile Trp Asn Arg Glu Leu Val Lys Pro Glu His
 115 120 125
 Cys Met Pro Phe Arg Met Ser His Leu Gln Ile Ile His Ala Pro Leu
 130 135 140
 Ile Glu Glu Lys Phe Val Gln Thr Ser Leu Val Ile Asn Phe Glu Ile
 145 150 155 160
 Ile Asn His Ile Arg Gln Arg Ile Met Glu Glu Cys Lys Glu Ser Phe
 165 170 175
 Ser Ser Phe Glu Ile Val Ala Ala Leu Val Trp Leu Ala Lys Ile Lys
 180 185 190
 Ala Phe Gln Ile Pro His Ser Glu Asn Val Lys Leu Leu Phe Ala Met
 195 200 205
 Asp Leu Arg Arg Ser Phe Asn Pro Pro Leu Pro His Gly Tyr Tyr Gly
 210 215 220
 Asn Ala Phe Gly Ile Ala Cys Ala Met Asp Asn Val His Asp Leu Leu
 225 230 235 240
 Ser Gly Ser Leu Leu Arg Ala Ile Met Ile Ile Lys Lys Ser Lys Phe
 245 250 255
 Ser Leu His Lys Glu Leu Asn Ser Lys Thr Val Met Ser Pro Ser Val
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<213> *Taxus cuspidata*

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<213> *Taxus cuspidata*

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 35 40 45

Phe Gln Gln Leu Leu Phe Ser Leu Pro Gln Asp Thr Asp Ile Glu Asp
 50 55 60

Leu His Leu Leu Ile Val Gln Val Thr His Phe Thr Cys Gly Asp Phe
 65 70 75 80

Val Val Gly Ala Asn Val Tyr Gly Ser Val Cys Asp Gly Lys Gly Phe
 85 90 95

Gly Gln Phe Leu Gln Gly Met Ala Glu Met Ala Arg Gly Glu Val Lys
 100 105 110

Pro Ser Ile Glu Pro Ile Trp Asn Arg Glu Leu Val Lys Pro Glu Asp
 115 120 125

Leu Met Ala Leu His Val Asp His Leu Arg Ile Ile His Thr Pro Leu
 130 135 140

Ile Glu Glu Lys Phe Val Gln Thr Ser Leu Val Ile Asn Phe Glu Ile
 145 150 155 160

Ile Asn His Ile Arg Arg Cys Ile Met Glu Glu Cys Lys Glu Ser Phe
 165 170 175

Ser Ser Phe Glu Ile Val Ala Ala Leu Val Trp Leu Ala Lys Ile Lys
 180 185 190

Ala Phe Arg Ile Pro His Ser Glu Asn Val Lys Ile Leu Phe Ala Met
 195 200 205

Asp Val Arg Arg Ser Phe Lys Pro Pro Leu Pro Lys Gly Tyr Tyr Gly
 210 215 220

Asn Ala Tyr Gly Ile Ala Cys Ala Met Asp Asn Val Gln Asp Leu Leu
 225 230 235 240

Ser Gly Ser Leu Leu His Ala Ile Met Ile Ile Lys Lys Ser Lys Phe
 245 250 255

Ser Leu His Lys Lys Ile Asn Ser Lys Thr Val Met Ser Pro Ser Pro
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Leu Asp Val Asn Met Lys Phe Glu Asn Val Val Ser Ile Thr Asp Trp

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      20           25           30

Asp Asn Asp Leu Ser Ala Val Arg Asp Leu Asp Glu Tyr Asn Pro Leu
      35           40           45

Phe Arg Gln Leu Gln Ser Thr Leu Pro Leu Asp Thr Asp Cys Lys Asp
      50           55           60

Leu His Leu Met Thr Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe
      65           70           75           80

Val Met Gly Thr Ser Val His Gln Ser Ile Cys Asp Gly Asn Gly Leu
      85           90           95

Gly Gln Phe Phe Lys Ser Met Ala Glu Met Val Arg Gly Glu Val Lys
      100          105          110

Pro Ser Ile Glu Pro Val Trp Asn Arg Glu Leu Val Lys Pro Glu Asp
      115          120          125

Tyr Ile His Leu Gln Leu Tyr Ile Gly Glu Phe Ile Arg Pro Pro Leu
      130          135          140

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Ala Phe Glu Lys Val Gly Gln Thr Ser Leu Ile Ile Ser Phe Glu Lys
145 150 155 160

Ile Asn His Ile Lys Arg Cys Ile Met Glu Glu Ser Lys Glu Ser Phe
165 170 175

Ser Ser Phe Glu Ile Val Thr Ala Leu Val Trp Leu Ala Arg Thr Arg
180 185 190

Ala Phe Gln Ile Pro His Asn Glu Asp Val Thr Leu Leu Leu Ala Met
195 200 205

Asp Ala Arg Arg Ser Phe Asp Pro Pro Ile Pro Lys Gly Tyr Tyr Gly
210 215 220

Asn Val Ile Gly Thr Ala Cys Ala Thr Asn Asn Val His Asn Leu Leu
225 230 235 240

Ser Gly Ser Leu Leu His Ala Leu Thr Ile Ile Lys Lys Ser Met Ser
245 250 255

Ser Phe Tyr Glu Asn Ile Thr Ser Arg Val Leu Val Asn Pro Ser Thr
260 265 270

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 35 40 45
 Leu Glu Gln Leu Leu Phe Cys Leu Pro Pro Asp Thr Asp Ile Glu Asp
 50 55 60
 Ile His Pro Leu Val Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe
 65 70 75 80
 Val Val Gly Val Ser Phe Cys His Gly Ile Cys Asp Gly Leu Gly Ala
 85 90 95
 Gly Gln Phe Leu Ile Ala Met Gly Glu Met Ala Arg Gly Glu Ile Lys
 100 105 110
 Pro Ser Ser Glu Pro Ile Trp Lys Arg Glu Leu Leu Lys Pro Glu Asp
 115 120 125
 Pro Leu Tyr Arg Phe Gln Tyr Tyr His Phe Gln Leu Ile Cys Pro Pro
 130 135 140
 Ser Thr Phe Gly Lys Ile Val Gln Gly Ser Leu Val Ile Thr Ser Glu
 145 150 155 160
 Thr Ile Asn Cys Ile Lys Gln Cys Leu Arg Glu Glu Ser Lys Glu Phe
 165 170 175
 Cys Ser Ala Phe Glu Val Val Ser Ala Leu Ala Trp Ile Ala Arg Thr
 180 185 190
 Arg Ala Leu Gln Ile Pro His Ser Glu Asn Val Lys Leu Ile Phe Ala
 195 200 205
 Met Asp Met Arg Lys Leu Phe Asn Pro Pro Leu Ser Lys Gly Tyr Tyr
 210 215 220
 Gly Asn Phe Val Gly Thr Val Cys Ala Met Asp Asn Val Lys Asp Leu
 225 230 235 240
 Leu Ser Gly Ser Leu Leu Arg Val Val Arg Ile Ile Lys Lys Ala Lys
 245 250 255
 Val Ser Leu Asn Glu His Phe Thr Ser Thr Ile Val Thr Pro Arg Ser
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<213> *Taxus cuspidata*

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          35           40           45
Phe Gln Gln Leu Ile Phe Ser Leu Pro Gln Asp Thr Asp Ile Glu Asp
          50           55           60
Leu His Leu Leu Ile Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe
          65           70           75           80
Val Val Gly Ala Asn Val Tyr Gly Ser Thr Cys Asp Ala Lys Gly Phe
          85           90           95
Gly Gln Phe Leu Gln Gly Met Ala Glu Met Ala Arg Gly Glu Val Lys
          100          105          110
Pro Ser Ile Glu Pro Ile Trp Asn Lys Arg Thr Gly Glu Ala Arg Arg
          115          120          125
Glu Val Lys Pro Ser Ile Glu Pro Ile Trp Asn Lys Arg Thr Gly Glu
          130          135          140
Ala Arg Arg Leu Tyr Ala Leu Ser Gly Met Ser His Leu Gln Ile Ile
          145          150          155          160
His Ala Pro Val Ile Glu Glu Lys Phe Val Gln Thr Ser Leu Val Ile
          165          170          175
Asn Phe Glu Ile Ile Asn His Ile Arg Arg Arg Ile Met Glu Glu Cys
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180 185 190
 Lys Glu Ser Leu Ser Ser Phe Glu Ile Val Ala Ala Leu Val Trp Leu
 195 200 205
 Ala Lys Ile Lys Ala Phe Gln Ile Pro His Ser Glu Asn Val Lys Leu
 210 215 220
 Leu Phe Ala Met Asp Leu Arg Arg Ser Phe Asn Pro Pro Leu Pro His
 225 230 235 240
 Gly Tyr Tyr Gly Asn Ala Phe Gly Ile Ala Cys Ala Met Asp Asn Val
 245 250 255
 His Asp Leu Leu Ser Gly Ser Leu Leu Arg Thr Ile Met Ile Ile Lys
 260 265 270
 Lys Ser Lys Phe Ser Leu His Lys Glu Leu Asn Ser Lys Thr Val Met
 275 280 285
 Ser Ser Ser Val Val Asp Val Asn Thr Lys Phe Glu Asp Val Val Ser
 290 295 300
 Ile Ser Asp Trp Arg His Ser Ile Tyr Tyr Glu Val Asp Phe Gly Trp
 305 310 315 320

Gly Lys

<210> 15
 <211> 908
 <212> DNA
 <213> *Taxus cuspidata*

<400> 15
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 gatttgatg ctcataatcc ttcatttcac cagctttctg tttcacctec agtggattot 180
 gatattgagg gcctccatct tgcagctctt caggtaactc gttttacatg tgggggtttt 240
 gttctaggag taagtttgaa ccaaagtgtg tgcgatggaa aaggattggg aaattttctt 300
 aaaggtgtgg cagagatggt gaggggaaaa gataagccct caattgaacc agtatggaat 360
 agagaaatgg taaagtttga agactataca cgcctccaat tttatcacca tgaattcata 420
 caaccacctt taatagatga gaaaattgtt caaaaatctc ttgttataaa cttggagaca 480
 ataaatatta tcaaacgatg tattatggaa gaatatacaa aattttttctc tacattcgaa 540
 atcgtagcag caatgggttg gctagcaaga acaaaaagctt tcaaaattcc acatagtga 600
 aatgcagagc ttctctttac aatggatatg agggaaatcat ttaatcccc tcttccaaag 660
 ggatactatg gtaatgttat gggtatagta tgtgcattgg ataattgtcaa acacctatta 720
 agtggatcta ttttgctgct tgcaatggtt atacagaaat caagggtttt ctttacagag 780
 aatttcoggt taagatctat gacacaacca tctgcattga ctgtgaagat caagcacaaa 840
 aatgtagttg catgtagtga ttggaggcaa tatggatatg atgaagtgga cttcggctgg 900
 ggtaaacc 908

<210> 16
 <211> 302
 <212> PRT
 <213> *Taxus cuspidata*

<400> 16
 Phe Tyr Pro Phe Ala Gly Arg Leu Arg Asn Lys Glu Asn Gly Asp Leu
 1 5 10 15

Glu Val Glu Cys Thr Gly Glu Gly Ala Val Phe Val Glu Ala Met Ala
 20 25 30
 Asp Thr Asp Leu Ser Ser Leu Gly Asp Leu Asp Ala His Asn Pro Ser
 35 40 45
 Phe His Gln Leu Ser Val Ser Pro Pro Val Asp Ser Asp Ile Glu Gly
 50 55 60
 Leu His Leu Ala Ala Leu Gln Val Thr Arg Phe Thr Cys Gly Gly Phe
 65 70 75 80
 Val Leu Gly Val Ser Leu Asn Gln Ser Val Cys Asp Gly Lys Gly Leu
 85 90 95
 Gly Asn Phe Leu Lys Gly Val Ala Glu Met Val Arg Gly Lys Asp Lys
 100 105 110
 Pro Ser Ile Glu Pro Val Trp Asn Arg Glu Met Val Lys Phe Glu Asp
 115 120 125
 Tyr Thr Arg Leu Gln Phe Tyr His His Glu Phe Ile Gln Pro Pro Leu
 130 135 140
 Ile Asp Glu Lys Ile Val Gln Lys Ser Leu Val Ile Asn Leu Glu Thr
 145 150 155 160
 Ile Asn Ile Ile Lys Arg Cys Ile Met Glu Glu Tyr Thr Lys Phe Phe
 165 170 175
 Ser Thr Phe Glu Ile Val Ala Ala Met Val Trp Leu Ala Arg Thr Lys
 180 185 190
 Ala Phe Lys Ile Pro His Ser Glu Asn Ala Glu Leu Leu Phe Thr Met
 195 200 205
 Asp Met Arg Glu Ser Phe Asn Pro Pro Leu Pro Lys Gly Tyr Tyr Gly
 210 215 220
 Asn Val Met Gly Ile Val Cys Ala Leu Asp Asn Val Lys His Leu Leu
 225 230 235 240
 Ser Gly Ser Ile Leu Arg Ala Ala Met Val Ile Gln Lys Ser Arg Phe
 245 250 255
 Phe Phe Thr Glu Asn Phe Arg Leu Arg Ser Met Thr Gln Pro Ser Ala
 260 265 270
 Leu Thr Val Lys Ile Lys His Lys Asn Val Val Ala Cys Ser Asp Trp
 275 280 285
 Arg Gln Tyr Gly Tyr Asp Glu Val Asp Phe Gly Trp Gly Lys
 290 295 300

<210> 17

<211> 908

<212> DNA

<213> *Taxus cuspidata*

<400> 17

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ggtttttgatt accacaatcc agcatttggg aagctacttt actcactacc actggatacc 180
cctatttcacg acctccatcc tctgggtgtt caggtaactc gttttacctg cgggggggtt 240
gttgtgggat taagtttgga ccatactata tgtgatggac gtggtgcagg tcaatttctt 300
aaagccctag cagaratggc gaggggagag gctaagccct cattggaacc aatatggaat 360
agagagtgtg tgaagccoga agaccttata cgcttgaat tttatcactt tgaatcgatg 420
cgtccacctc caatagttga agaaatggtt caatcatcta ttattataaa tgctgagaca 480
ataagtaata tsaaacaata cattatggaa gaatgtaaag aatcttggtc tgcatttgat 540
gtcgtaggag gattggcttg gctagccagg acaaaggctt ttcaaattcc acatacagag 600
aatgtgatgg ttattttttgc agtggatgag aggagatcat ttgatccacc acttccaaag 660
ggttactatg gtaatgtcgt tggtaatgca tgtgcattgg ataatgttca agacctotta 720
aatggatctc ttttgcggtc tacaatgatt ataaagaaat caaaggatc tttaaaagag 780
aatataaggg caaaaacttt gacgatacca tctatagtag atgtgaatgt gaaacatgaa 840
aacatagttg gattaggcga tttgagacga ctgggattta atgaagtgga cttcggctgg 900
ggsaagcc                                     908
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<210> 18

<211> 302

<212> PRT

<213> *Taxus cuspidata*

<400> 18

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Phe Tyr Pro Phe Ala Gly Arg Met Arg Asn Lys Gly Asp Gly Glu Leu
  1             5             10             15

Glu Val Asp Cys Thr Gly Glu Gly Ala Leu Phe Val Glu Ala Met Ala
      20             25             30

Asp Asp Asn Leu Ser Val Leu Gly Gly Phe Asp Tyr His Asn Pro Ala
      35             40             45

Phe Gly Lys Leu Leu Tyr Ser Leu Pro Leu Asp Thr Pro Ile His Asp
      50             55             60

Leu His Pro Leu Val Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe
      65             70             75             80

Val Val Gly Leu Ser Leu Asp His Thr Ile Cys Asp Gly Arg Gly Ala
      85             90             95

Gly Gln Phe Leu Lys Ala Leu Ala Glu Met Ala Arg Gly Glu Ala Lys
      100            105            110

Pro Ser Leu Glu Pro Ile Met Asn Arg Glu Leu Leu Lys Pro Glu Asp
      115            120            125

Leu Ile Arg Leu Gln Phe Tyr His Phe Glu Ser Met Arg Pro Pro Pro
      130            135            140

Ile Val Glu Glu Met Val Gln Ser Ser Ile Ile Ile Asn Ala Glu Thr
      145            150            155            160

Ile Ser Asn Xaa Lys Gln Tyr Ile Met Glu Glu Cys Lys Glu Ser Cys
      165            170            175

Ser Ala Phe Asp Val Val Gly Gly Leu Ala Met Leu Ala Arg Thr Lys
      180            185            190

Ala Phe Gln Ile Pro His Thr Glu Asn Val Met Val Ile Phe Ala Val
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195 200 205

Asp Ala Arg Arg Ser Phe Asp Pro Pro Leu Pro Lys Gly Tyr Tyr Gly
210 .. 215 220

Asn Val Val Gly Asn Ala Cys Ala Leu Asp Asn Val Gln Asp Leu Leu
225 230 235 240

Asn Gly Ser Leu Leu Arg Ala Thr Met Ile Ile Lys Lys Ser Lys Val
245 250 255

Ser Leu Lys Glu Asn Ile Arg Ala Lys Thr Leu Thr Ile Pro Ser Ile
260 265 270

Val Asp Val Asn Val Lys His Glu Asn Ile Val Gly Leu Gly Asp Leu
275 280 285

Arg Arg Leu Gly Phe Asn Glu Val Asp Phe Gly Trp Gly Lys
290 295 300

<210> 19
<211> 911
<212> DNA
<213> *Taxus cuspidata*

<400> 19
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gatctggatg acctcaatcc atcatttcag cagttagttt tttggcatcc attggacact 180
gctattgagg atcttcatct tgtgattgtt caggtaacac gttttacatg tgggggcatt 240
gccgttgagg tgaactttgcc ccatagtgta tgtgatggac gtggagcaacc ccagtttgtt 300
acagcactgg cagaaatggc gaggggagag gttaagccct tattagaacc aatatggaat 360
agagaattgt tgaaccctga agaccctcta catctccagt taaatcaatt tgattcgata 420
tgcccacctc caatgctcga ggaattgggt caagcttctt ttgttataaa tgttgacacc 480
atagaatata tgaacaatg tgttatggag gaatgtaatg atttttgttc gtcctttgaa 540
gtagtggcag cattggtttg gatagcaagg acaaaggctc ttcaaattcc acatactgag 600
aatgtgaagc ttctctttgc gatggatttg aggaaattat ttaatccccc acttccaaat 660
ggatattatg gtaatgccat tggtagtcca tatgcaatgg ataattgtca agacctctta 720
aatggatctc ttttgctgac tataatgatt ataaaaaaag caaaggctga tttaaaagat 780
aattattcga ggtcaagggt agttacaaac ccaaattcat tagatgtgaa caagaaatcc 840
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tggggcaagc c 911

<210> 20
<211> 303
<212> PRT
<213> *Taxus cuspidata*

<400> 20
Tyr Tyr Pro Leu Ala Gly Arg Leu Arg Ser Lys Glu Ile Gly Glu Leu
1 5 10 15

Glu Val Glu Cys Thr Gly Asp Gly Ala Leu Phe Val Glu Ala Met Val
20 25 30

Glu Asp Thr Ile Ser Val Leu Arg Asp Leu Asp Asp Leu Asn Pro Ser
35 40 45

Phe Gln Gln Leu Val Phe Trp His Pro Leu Asp Thr Ala Ile Glu Asp
50 55 60

Leu His Leu Val Ile Val Gln Val Thr Arg Phe Thr Cys Gly Gly Ile
 65 70 75 80
 Ala Val Gly Val Thr Leu Pro His Ser Val Cys Asp Gly Arg Gly Ala
 85 90 95
 Pro Gln Phe Val Thr Ala Leu Ala Glu Met Ala Arg Gly Glu Val Lys
 100 105 110
 Pro Leu Leu Glu Pro Ile Trp Asn Arg Glu Leu Leu Asn Pro Glu Asp
 115 120 125
 Pro Leu His Leu Gln Leu Asn Gln Phe Asp Ser Ile Cys Pro Pro Pro
 130 135 140
 Met Leu Glu Glu Leu Gly Gln Ala Ser Phe Val Ile Asn Val Asp Thr
 145 150 155 160
 Ile Glu Tyr Met Lys Gln Cys Val Met Glu Glu Cys Asn Asp Phe Cys
 165 170 175
 Ser Ser Phe Glu Val Val Ala Ala Leu Val Trp Ile Ala Arg Thr Lys
 180 185 190
 Ala Leu Gln Ile Pro His Thr Glu Asn Val Lys Leu Leu Phe Ala Met
 195 200 205
 Asp Leu Arg Lys Leu Phe Asn Pro Pro Leu Pro Asn Gly Tyr Tyr Gly
 210 215 220
 Asn Ala Ile Gly Thr Ala Tyr Ala Met Asp Asn Val Gln Asp Leu Leu
 225 230 235 240
 Asn Gly Ser Leu Leu Arg Ala Ile Met Ile Ile Lys Lys Ala Lys Ala
 245 250 255
 Asp Leu Lys Asp Asn Tyr Ser Arg Ser Arg Val Val Thr Asn Pro Asn
 260 265 270
 Ser Leu Asp Val Asn Lys Lys Ser Asn Asn Ile Leu Ala Leu Ser Asp
 275 280 285
 Trp Arg Arg Leu Gly Phe Tyr Glu Ala Asp Phe Gly Trp Gly Lys
 290 295 300

<210> 21
 <211> 911
 <212> DNA
 <213> *Taxus cuspidata*

<400> 21
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 gatctggatg acctcaatcc atcatttcag cagtttagttt tttggcatcc attggacact 180
 gctattgagg atcttcatct tgtgattgtt caggtaacac gttttacatg tgggggcatt 240
 gccgttggag tgactttgccc ccatagtgtg tgtgatggac gtggagcacc ccagtttgtt 300
 acagcactgg cagaaatggc gaggggagag gttaagccct tattagaacc aatatggaat 360
 agagaattgt tgaaccctga agaccctcta catctccagt taaatcaatt tgattcgata 420
 tgcccacctc caatgctcga ggaattgggt caagcttctt ttgttataaa tgttgacacc 480

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atagaatata tgaacaatg tgttatggag gaatgtaatg atttttgttc gtcctttgaa 540
gtagtggcag cattggtttg gatagcaagg acaaaggctc ttcaaattcc acatactgag 600
aatgtgaagc ttctctttgc gatggatttg aggaaattat ttaatccccc acttccaaat 660
ggatattatg gtaatgccat tggactgca tatgcaatgg ataatgtcca agacctctta 720
aatggatctc ttttgcgtgc tataatgatt ataaaaaaag caaaggctga tttaaaagat 780
aattattcga ggtcaagggt agttacaaac ccaaattcat tagatgtgaa caagaaatcc 840
aacaacattc ttgcattgag tgactggagg cggttgggat tttatgaagc cgattttggc 900
tggggcaagc c 911

```

<210> 22

<211> 306

<212> PRT

<213> *Taxus cuspidata*

<400> 22

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Tyr Tyr Pro Leu Ala Gly Arg Leu Glu Thr Cys Asp Gly Met Val Tyr
  1              5              10              15

```

```

Ile Asp Cys Asn Asp Lys Gly Ala Glu Phe Ile Glu Ala Tyr Ala Ser
          20              25              30

```

```

Pro Glu Leu Gly Val Ala Glu Ile Met Ala Asp Ser Phe Pro His Gln
          35              40              45

```

```

Ile Phe Ala Phe Asn Gly Val Leu Asn Ile Asp Gly His Phe Met Pro
          50              55              60

```

```

Leu Leu Ala Val Gln Ala Thr Lys Leu Lys Asp Gly Ile Ala Leu Ala
          65              70              75              80

```

```

Ile Thr Val Asn His Ala Val Ala Asp Ala Thr Ser Val Trp His Phe
          85              90              95

```

```

Ile Ser Ser Trp Ala Gln Leu Cys Lys Glu Pro Ser Asn Ile Pro Leu
          100             105             110

```

```

Leu Pro Leu His Thr Arg Cys Phe Thr Thr Ile Ser Pro Ile Lys Leu
          115             120             125

```

```

Asp Ile Gln Tyr Ser Ser Thr Thr Thr Glu Ser Ile Asp Asn Phe Phe
          130             135             140

```

```

Pro Pro Pro Leu Thr Glu Lys Ile Phe His Phe Ser Gly Lys Thr Ile
          145             150             155             160

```

```

Ser Arg Leu Lys Glu Glu Ala Met Glu Ala Cys Lys Asp Lys Ser Ile
          165             170             175

```

```

Ser Ile Ser Ser Phe Gln Ala Leu Cys Gly His Leu Trp Gln Ser Ile
          180             185             190

```

```

Thr Arg Ala Arg Gly Leu Ser Pro Ser Glu Pro Thr Thr Ile Lys Ile
          195             200             205

```

```

Ala Val Asn Cys Arg Pro Arg Ile Val Pro Pro Leu Pro Asn Ser Tyr
          210             215             220

```

```

Phe Gly Asn Ala Val Gln Val Val Asp Val Thr Met Thr Thr Glu Glu
          225             230             235             240

```

```

Leu Leu Gly Asn Gly Gly Ala Cys Ala Ala Leu Ile Leu His Gln Lys

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245

250

255

Ile Ser Ala His Gln Asp Thr Gln Ile Arg Ala Glu Leu Asp Lys Pro
 .. 260 265 270

Pro Lys Ile Val His Thr Asn Asn Leu Ile Pro Cys Asn Ile Ile Ala
 275 280 285

Met Ala Gly Ser Pro Arg Phe Pro Ile Tyr Asn Asn Asp Phe Gly Trp
 290 295 300

Gly Lys
 305

<210> 23

<211> 908

<212> DNA

<213> Taxus cuspidata

<400> 23

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acaggggagg gtgcactgtt tgtggaagcc gtggtggaca atgatctttc agtcttgaaa 120
gatttggatg cccaaaatgc atcttatgag cagttgctct tttcgcttcc gcccaataca 180
caggttcagg acctccatcc tctgattctt caggtaactc gttttaaatg tggagggttt 240
gttgtgggag ttggtttcca ccatagtata tgtgacgcac gaggaggaac tcaatttctt 300
ctaggcctag cagatatggc aaggggagag actaagcctt tagtggaacc agtatggaat 360
agagaactga taaacctga agatctaata cacctccaat ttcataagtt tggtttgata 420
cgccaacctc taaaacttga tgaaatttgt caagcatctt ttactataaa ctcaaagata 480
ataaattaca tcaaacaatg tgttatagaa gaatgtaatg aaattttctc tgcatttgaa 540
gttgtagtag cattaacttg gatagcaagg acaaaggctt ttcaaattcc acatagttag 600
aatgtgatga tgctcttttg aatggacgcg aggaaatatt ttaatccccc acttccaaag 660
ggatattatg gtaatgccat tggacttca tgtgtaattg aaaatgtaca agacctctta 720
aatggatctc tttcgctgac tgtaatgac acaaagaaat caaagggtccc tttaattgag 780
aatttaaggt caagaattgt ggcgaaacaa tctggagtag atgaggaaat taagcatgaa 840
aacgtagttg gatttggaga ttggaggcga ttgggatttc atgaagtgga cttcggctgg 900
ggcaagcc . 908

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<210> 24

<211> 302

<212> PRT

<213> Taxus cuspidata

<400> 24

Phe Tyr Pro Phe Ala Gly Arg Ile Arg Gln Lys Glu Asn Glu Glu Leu
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Glu Val Glu Cys Thr Gly Glu Gly Ala Leu Phe Val Glu Ala Val Val
 20 25 30

Asp Asn Asp Leu Ser Val Leu Lys Asp Leu Asp Ala Gln Asn Ala Ser
 35 40 45

Tyr Glu Gln Leu Leu Phe Ser Leu Pro Pro Asn Thr Gln Val Gln Asp
 50 55 60

Leu His Pro Leu Ile Leu Gln Val Thr Arg Phe Lys Cys Gly Gly Phe
 65 70 75 80

Val Val Gly Val Gly Phe His His Ser Ile Cys Asp Ala Arg Gly Gly
 85 90 95

Thr Gln Phe Leu Leu Gly Leu Ala Asp Met Ala Arg Gly Glu Thr Lys
 100 105 110
 Pro Leu Val Glu Pro Val Trp Asn Arg Glu Leu Ile Asn Pro Glu Asp
 115 120 125
 Leu Met His Leu Gln Phe His Lys Phe Gly Leu Ile Arg Gln Pro Leu
 130 135 140
 Lys Leu Asp Glu Ile Cys Gln Ala Ser Phe Thr Ile Asn Ser Lys Ile
 145 150 155 160
 Ile Asn Tyr Ile Lys Gln Cys Val Ile Glu Glu Cys Asn Glu Ile Phe
 165 170 175
 Ser Ala Phe Glu Val Val Val Ala Leu Thr Trp Ile Ala Arg Thr Lys
 180 185 190
 Ala Phe Gln Ile Pro His Ser Glu Asn Val Met Met Leu Phe Gly Met
 195 200 205
 Asp Ala Arg Lys Tyr Phe Asn Pro Pro Leu Pro Lys Gly Tyr Tyr Gly
 210 215 220
 Asn Ala Ile Gly Thr Ser Cys Val Ile Glu Asn Val Gln Asp Leu Leu
 225 230 235 240
 Asn Gly Ser Leu Ser Arg Ala Val Met Ile Thr Lys Lys Ser Lys Val
 245 250 255
 Pro Leu Ile Glu Asn Leu Arg Ser Arg Ile Val Ala Asn Gln Ser Gly
 260 265 270
 Val Asp Glu Glu Ile Lys His Glu Asn Val Val Gly Phe Gly Asp Trp
 275 280 285
 Arg Arg Leu Gly Phe His Glu Val Asp Phe Gly Trp Gly Lys
 290 295 300

<210> 25
 <211> 1320
 <212> DNA
 <213> *Taxus cuspidata*

<400> 25
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 ttatcagttc acaatgcctc ccagagaggt tctgtttctg cagatcctgc aaaaacaatt 180
 cgagaggctc tctccaaggt gctggtttat tatccccctt ttgctggaag gctgagaaac 240
 acagaaaatg gggatcctga agtggagtgc acaggggagg gtgccgtctt tgtggaagcc 300
 atggcggaca acgaccttc agtattacaa gatttcaatg agtacgatcc atcatttcag 360
 cagctagttt ttaatcttcg agaggatgtc aatattgagg acctccatct tctaactgtt 420
 caggtaaact gttttacatg tggaggattt gttgtgggca caagattcca ccatagtgtg 480
 tctgatggaa aaggaatcgg ccagttactt aaaggcatgg gagagatggc aaggggggag 540
 ttttaagcct cgttagaacc aatatggaat agagaaatgg tgaagcctga agacattatg 600
 tacctccagt ttgatcactt tgatttcata caccacactc ttaatcttga gaagtctatt 660
 caagcatcta tggttaataag ctttgagaga ataaattata tcaaacgatg catgatggaa 720
 gaatgcaaag aatttttttc tgcatttgaa gttgtagtag cattgatttg gctggcaagg 780
 acaaagtctt ttcgaattcc acccaatgag tatgtgaaaa ttatctttcc aatcgacatg 840

	245		250		255										
Trp	Leu	Ala	Arg	Thr	Lys	Ser	Phe	Arg	Ile	Pro	Pro	Asn	Glu	Tyr	Val
			260					265					270		
Lys	Ile	Ile	Phe	Pro	Ile	Asp	Met	Arg	Asn	Ser	Phe	Asp	Ser	Pro	Leu
		275					280					285			
Pro	Lys	Gly	Tyr	Tyr	Gly	Asn	Ala	Ile	Gly	Asn	Ala	Cys	Ala	Met	Asp
	290					295					300				
Asn	Val	Lys	Asp	Leu	Leu	Asn	Gly	Ser	Leu	Leu	Tyr	Ala	Leu	Met	Leu
305					310					315					320
Ile	Lys	Lys	Ser	Lys	Phe	Ala	Leu	Asn	Glu	Asn	Phe	Lys	Ser	Arg	Ile
				325					330					335	
Leu	Thr	Lys	Pro	Ser	Thr	Leu	Asp	Ala	Asn	Met	Lys	His	Glu	Asn	Val
			340					345					350		
Val	Gly	Cys	Gly	Asp	Trp	Arg	Asn	Leu	Gly	Phe	Tyr	Glu	Ala	Asp	Phe
		355					360					365			
Gly	Trp	Gly	Asn	Ala	Val	Asn	Val	Ser	Pro	Met	Gln	Gln	Gln	Arg	Glu
	370					375					380				
His	Glu	Leu	Ala	Met	Gln	Asn	Tyr	Phe	Leu	Phe	Leu	Arg	Ser	Ala	Lys
385					390					395					400
Asn	Met	Ile	Asp	Gly	Ile	Lys	Ile	Leu	Met	Phe	Met	Pro	Ala	Ser	Met
				405					410					415	
Val	Lys	Pro	Phe	Lys	Ile	Glu	Met	Glu	Val	Thr	Ile	Asn	Lys	Tyr	Val
		420						425					430		
Ala	Lys	Ile	Cys	Asn	Ser	Lys	Leu								
	435						440								

<210> 27
 <211> 1317
 <212> DNA
 <213> Taxus cuspidata

<400> 27
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 agcatttttca atgccttggt aattttacaat gcctctccct ctcccaccat gatctctgca 180
 gatcctgcaa aaccaattag agaagctctc gccaaagatcc tggtttatta tccccctttt 240
 gctgggcgcc tcagagagac agaaaatggg gatctggaag tggaaatgcac aggggagggg 300
 gctatgtttt tggaagccat ggcagacaat gagctgtctg tgttgggaga ttttgatgac 360
 agcaatccat catttcagca gctacttttt tcgcttcac tcgataccaa tttcaaagac 420
 ctctctcttc tggttgttca ggtaactcgt tttacatgtg gaggccttgt tgttgagtg 480
 agtttccacc atgggtgtat tgatggtcga ggagcggccc aatttcttaa aggtttggca 540
 gagatggcac ggggagaggt taagctctca ttggaaccaa tatggaatag ggaactagt 600
 aagcttgatg accctaaata cttcaattt tttcactttg aattcctacg agcgccttca 660
 attgttgaga aaattgttca aacatatttt attatagatt ttgagaccat aaattatata 720
 aaacaatctg ttatggaaga atgtaaagaa ttttgctctt cattogaagt tgcacagca 780
 atgacttgga tagcaaggac aagagctttt caaattccag aaagttagta cgtgaaaatt 840
 ctcttcggaa tggacatgag gaactcattt aatccccctc ttccaagcgg atactatggt 900
 aactocattg gtaccgcatg tgcagtggat aatgttcaag acctcttaag tggatctctt 960

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ttgcgtgcta taatgattat aaagaaatca aaggtctott taaatgataa tttcaagtca 1020
agagctgtgg tgaagccatc tgaattggat gtgaatatga atcatgaaaa cgtagttgca 1080
tttgctgatt ggagccgatt gggatttgat gaagtggatt ttggttgggg gaatgcggtg 1140
agtgtaaacc ctgtgcaaca acagtctgcg ttagcaatgc aaaattattt tcttttccta 1200
aaaccttcca agaacaagcc cgatggaatc aaaatattaa tgtttctgcc cctatcaaaa 1260
atgaagtcac tcaaaattga aatggaagcc atgatgaaaa aatatgtggc taaagta 1317

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<210> 28

<211> 439

<212> PRT

<213> Artificial Sequence

<400> 28

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Met Glu Lys Thr Asp Leu His Val Asn Leu Ile Glu Lys Val Met Val
  1             5             10             15

```

```

Gly Pro Ser Pro Pro Leu Pro Lys Thr Thr Leu Gln Leu Ser Ser Ile
          20             25             30

```

```

Asp Asn Leu Pro Gly Val Arg Gly Ser Ile Phe Asn Ala Leu Leu Ile
          35             40             45

```

```

Tyr Asn Ala Ser Pro Ser Pro Thr Met Ile Ser Ala Asp Pro Ala Lys
          50             55             60

```

```

Pro Ile Arg Glu Ala Leu Ala Lys Ile Leu Val Tyr Tyr Pro Pro Phe
          65             70             75             80

```

```

Ala Gly Arg Leu Arg Glu Thr Glu Asn Gly Asp Leu Glu Val Glu Cys
          85             90             95

```

```

Thr Gly Glu Gly Ala Met Phe Leu Glu Ala Met Ala Asp Asn Glu Leu
          100            105            110

```

```

Ser Val Leu Gly Asp Phe Asp Asp Ser Asn Pro Ser Phe Gln Gln Leu
          115            120            125

```

```

Leu Phe Ser Leu Pro Leu Asp Thr Asn Phe Lys Asp Leu Ser Leu Leu
          130            135            140

```

```

Val Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val Val Gly Val
          145            150            155            160

```

```

Ser Phe His His Gly Val Cys Asp Gly Arg Gly Ala Ala Gln Phe Leu
          165            170            175

```

```

Lys Gly Leu Ala Glu Met Ala Arg Gly Glu Val Lys Leu Ser Leu Glu
          180            185            190

```

```

Pro Ile Trp Asn Arg Glu Leu Val Lys Leu Asp Asp Pro Lys Tyr Leu
          195            200            205

```

```

Gln Phe Phe His Phe Glu Phe Leu Arg Ala Pro Ser Ile Val Glu Lys
          210            215            220

```

```

Ile Val Gln Thr Tyr Phe Ile Ile Asp Phe Glu Thr Ile Asn Tyr Ile
          225            230            235            240

```

```

Lys Gln Ser Val Met Glu Glu Cys Lys Glu Phe Cys Ser Ser Phe Glu
          245            250            255

```

Val Ala Ser Ala Met Thr Trp Ile Ala Arg Thr Arg Ala Phe Gln Ile
 260 265 270
 Pro Glu Ser Glu Tyr Val Lys Ile Leu Phe Gly Met Asp Met Arg Asn
 275 280 285
 Ser Phe Asn Pro Pro Leu Pro Ser Gly Tyr Tyr Gly Asn Ser Ile Gly
 290 295 300
 Thr Ala Cys Ala Val Asp Asn Val Gln Asp Leu Leu Ser Gly Ser Leu
 305 310 315 320
 Leu Arg Ala Ile Met Ile Ile Lys Lys Ser Lys Val Ser Leu Asn Asp
 325 330 335
 Asn Phe Lys Ser Arg Ala Val Val Lys Pro Ser Glu Leu Asp Val Asn
 340 345 350
 Met Asn His Glu Asn Val Val Ala Phe Ala Asp Trp Ser Arg Leu Gly
 355 360 365
 Phe Asp Glu Val Asp Phe Gly Trp Gly Asn Ala Val Ser Val Ser Pro
 370 375 380
 Val Gln Gln Gln Ser Ala Leu Ala Met Gln Asn Tyr Phe Leu Phe Leu
 385 390 395 400
 Lys Pro Ser Lys Asn Lys Pro Asp Gly Ile Lys Ile Leu Met Phe Leu
 405 410 415
 Pro Leu Ser Lys Met Lys Ser Phe Lys Ile Glu Met Glu Ala Met Met
 420 425 430
 Lys Lys Tyr Val Ala Lys Val
 435

<210> 29
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:proteolytic
 fragment

<400> 29
 Thr Thr Leu Gln Leu Ser Ser Ile Asp Asn Leu Pro Gly Val Arg
 1 5 10 15

<210> 30
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:proteolytic
 fragment

<400> 30

Ile Leu Val Tyr Tyr Pro Pro Phe Ala Gly Arg
 1 5 10

<210> 31
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:proteolytic
 fragment

<400> 31
 Phe Thr Cys Gly Gly Phe Val Val Gly Val Ser Phe
 1 5 10

<210> 32
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:proteolytic
 fragment

<400> 32
 Lys Gly Leu Ala Glu Ile Ala Arg Gly Glu Val Lys
 1 5 10

<210> 33
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:proteolytic
 fragment

<400> 33
 Asn Leu Pro Asn Asp Thr Asn Pro Ser Ser Gly Tyr Tyr Gly Asn
 1 5 10 15

<210> 34
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR primer

<400> 34
 atnctngtnt attatccncc

20

<210> 35
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 35

tattatccnc cntttgcngg

20

<210> 36

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 36

ttctatccnt tcgcnggnag

20

<210> 37

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 37

tactatccnt tngcnggnag

20

<210> 38

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 38

ctaaaaccna ccccntttgg

20

<210> 39

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence

<400> 39

Phe Tyr Pro Phe Ala Gly Arg

1

5

<210> 40

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus

sequence

<400> 40

Tyr Tyr Pro Leu Ala Gly Arg
1 5

<210> 41

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:consensus
sequence

<400> 41

Asp Phe Gly Trp Gly Lys Pro
1 5

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 42

cctcatcttt cccccattga taat

24

<210> 43

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 43

aaaaagaaaa taattttgcc atgcaag

27

<210> 44

<211> 1320

<212> DNA

<213> Taxus cuspidata

<400> 44

atggcaggct	caacagaatt	tgtggtaaga	agcttagaga	gagtgatggt	ggctccaagc	60
cagccatcgc	ccaaagcttt	cctgcagctc	tccacccttg	acaatctacc	aggggtgaga	120
gaaaacattt	ttaacacctt	gttagtctac	aatgcctcag	acagagtttc	cgtagatcct	180
gcaaaagtaa	ttcggcaggc	tctctccaag	gtgttggtgt	actattcccc	ttttgcaggg	240
cgtctcagga	aaaaagaaaa	tggagatcct	gaagtggagt	gcacagggga	gggtgctctg	300
tttgtggaag	ccatggctga	cactgacctc	tcagtcttag	gagatttgga	tgactacagt	360
ccttcacttg	agcaactact	tttttgtctt	ccgcctgata	cagatattga	ggacatccat	420
cctctggtgg	ttcaggtaac	tcgtttttaca	tgtggagggt	ttgttgtagg	ggtgagtttc	480
tgccatggta	tatgtgatgg	actaggagca	ggccagtttc	ttatagccat	gggagagatg	540
gcaaggggag	agattaagcc	ctcctcggag	ccaatatgga	agagagaatt	gctgaagccg	600
gaagaccctt	tataccggtt	ccagtattat	cactttcaat	tgatttgccc	gccttcaaca	660
ttcgggaaaa	tagttcaagg	atctcttggt	ataacctctg	agacaataaa	ttgtatcaaa	720

caatgcctta gggaagaaaag taaagaattt tgctctgcgt tcgaagttgt atctgcattg 780
 gcttgatag caaggacaag ggctcttcaa attccacata gtgagaatgt gaagcttatt 840
 tttgcaatgg acatgagaaa attatttaatt ccaccacttt cgaagggata ctacggtaat 900
 tttgttggtta ccgtatgtgc aatggataat gtcaaggacc tattaagtgg atctcttttg 960
 cgtgttgtaa ggattataaaa gaaagcaaag gtctctttaa atgagcattt cacgtcaaca 1020
 atcgtgacac cccgttcttg atcagatgag agtatcaatt atgaaaacat agttggattt 1080
 ggtgatogaa ggcgattggg atttgatgaa gtagactttg ggtgggggca tgcagataat 1140
 gtaagtctcg tgcaacatgg attgaaggat gtttcagtcg tgcaaagtta ttttcttttc 1200
 atacgacctc ccaagaataa ccccgatgga atcaagatcc tatcgttcat gcccccgta 1260
 atagtgaat ccttcaaatt tgaaatggaa accatgacaa acaaatatgt aactaagcct 1320

<210> 45

<211> 440

<212> PRT

<213> *Taxus cuspidata*

<400> 45

Met Ala Gly Ser Thr Glu Phe Val Val Arg Ser Leu Glu Arg Val Met
 1 5 10 15

Val Ala Pro Ser Gln Pro Ser Pro Lys Ala Phe Leu Gln Leu Ser Thr
 20 25 30

Leu Asp Asn Leu Pro Gly Val Arg Glu Asn Ile Phe Asn Thr Leu Leu
 35 40 45

Val Tyr Asn Ala Ser Asp Arg Val Ser Val Asp Pro Ala Lys Val Ile
 50 55 60

Arg Gln Ala Leu Ser Lys Val Leu Val Tyr Tyr Ser Pro Phe Ala Gly
 65 70 75 80

Arg Leu Arg Lys Lys Glu Asn Gly Asp Leu Glu Val Glu Cys Thr Gly
 85 90 95

Glu Gly Ala Leu Phe Val Glu Ala Met Ala Asp Thr Asp Leu Ser Val
 100 105 110

Leu Gly Asp Leu Asp Asp Tyr Ser Pro Ser Leu Glu Gln Leu Leu Phe
 115 120 125

Cys Leu Pro Pro Asp Thr Asp Ile Glu Asp Ile His Pro Leu Val Val
 130 135 140

Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val Val Gly Val Ser Phe
 145 150 155 160

Cys His Gly Ile Cys Asp Gly Leu Gly Ala Gly Gln Phe Leu Ile Ala
 165 170 175

Met Gly Glu Met Ala Arg Gly Glu Ile Lys Pro Ser Ser Glu Pro Ile
 180 185 190

Trp Lys Arg Glu Leu Leu Lys Pro Glu Asp Pro Leu Tyr Arg Phe Gln
 195 200 205

Tyr Tyr His Phe Gln Leu Ile Cys Pro Pro Ser Thr Phe Gly Lys Ile
 210 215 220

Val Gln Gly Ser Leu Val Ile Thr Ser Glu Thr Ile Asn Cys Ile Lys
 225 230 235 240

Gln Cys Leu Arg Glu Glu Ser Lys Glu Phe Cys Ser Ala Phe Glu Val
 245 250 255
 Val Ser Ala Leu Ala Trp Ile Ala Arg Thr Arg Ala Leu Gln Ile Pro
 260 265 270
 His Ser Glu Asn Val Lys Leu Ile Phe Ala Met Asp Met Arg Lys Leu
 275 280 285
 Phe Asn Pro Pro Leu Ser Lys Gly Tyr Tyr Gly Asn Phe Val Gly Thr
 290 295 300
 Val Cys Ala Met Asp Asn Val Lys Asp Leu Leu Ser Gly Ser Leu Leu
 305 310 315 320
 Arg Val Val Arg Ile Ile Lys Lys Ala Lys Val Ser Leu Asn Glu His
 325 330 335
 Phe Thr Ser Thr Ile Val Thr Pro Arg Ser Gly Ser Asp Glu Ser Ile
 340 345 350
 Asn Tyr Glu Asn Ile Val Gly Phe Gly Asp Arg Arg Arg Leu Gly Phe
 355 360 365
 Asp Glu Val Asp Phe Gly Trp Gly His Ala Asp Asn Val Ser Leu Val
 370 375 380
 Gln His Gly Leu Lys Asp Val Ser Val Val Gln Ser Tyr Phe Leu Phe
 385 390 395 400
 Ile Arg Pro Pro Lys Asn Asn Pro Asp Gly Ile Lys Ile Leu Ser Phe
 405 410 415
 Met Pro Pro Ser Ile Val Lys Ser Phe Lys Phe Glu Met Glu Thr Met
 420 425 430
 Thr Asn Lys Tyr Val Thr Lys Pro
 435 440

<210> 46

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 46

gggaattcca tatggcaggc tcaacagaat ttgtgg

36

<210> 47

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 47

gtttatacat tgattcggaa ctagatctga tc

32

<210> 48

<211> 6 ..

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6 amino acid
motif found in acyl transferases

<220>

<221> VARIANT

<222> (2)..(4)

<223> Any amino acid

<400> 48

His Xaa Xaa Xaa Asp Gly
1 5

<210> 49

<211> 1332

<212> DNA

<213> *Taxus cuspidata*

<400> 49

```
atggagaagt ctggttcagc agatctacat gtaaatatca ttgagcgagt ggtggtggcg 60
ccatgccagc cgacgcccaa aacaatcctg cagctctcta gcattgacaa aatggggagga 120
ggatttgcca acgtattgct agtcttcggg gcctcccatg gcgtttctgc agatcctgca 180
aaaacaattc gagaggctct ctccaagacc ttggtctttt atttcccttt tgctgggagg 240
ctcagaaaaga aagaagatgg ggatatcgaa gtggagtgc tagagcagg agctctgttc 300
gtggaagcca tggcggacaa cgatctttca gtcgtacgag atctggatga gtacaatcca 360
ttatttcggc agctacaatc ttcgctttca ctggatacag attacaagga cctccatctt 420
atgactgttc aggtaaactcc gtttacatgt ggggggttttgc tcatgggaac gagtgtacac 480
caaagtatat gcgatggaaa tggattgggg caatttttta aaagcatggc agagatagtg 540
aggggagaag ttaagccctc aatcgaacca atatggaata gagaattggg gaagcctgaa 600
gactatatac acctccagtt gtatgtcagt gaattcattc gccaccttt agtagttgag 660
aaagtggggc aaacatctct tgttataagc ttcgagaaaa taaatcatat caaacgatgc 720
attatggaag aaagtaaaga atctttctct tcatttgaaa ttgtaacagc aatgggttgg 780
ctagcaagga caagggcttt tcaaattcca cacaacgagg atgtgactct tctccttgca 840
atggatgcaa ggagatcatt tgacccccct attccgaagg gatactacgg taatgtcatt 900
ggtactacat atgcaaaaaga taatgtccac aacctcttaa gtggatctct tttgcatgct 960
ctaacagtta taaagaaatc aatgtcctca ttttatgaga atatgacctc aagagtcttg 1020
gtgaacccat ctacattaga tttgagtatg aagtatgaaa atgtagtttc acttagtgat 1080
tggagccggg tgggacataa tgaagtggac tttgggtggg gaaatgcaat aaatgtaagc 1140
actctgcaac aacaatggga aaatgaggta gctataccaa ctttttttac tttccttcaa 1200
actcccaaga atataccaga tggaatcaag atactaatgt tcatgcccc atcaagagag 1260
aaaacattcg aaattgaagt ggaagccatg ataagaaaat atttgactaa agtgtcgcat 1320
tcaaagctat aa 1332
```

<210> 50

<211> 443

<212> PRT

<213> *Taxus cuspidata*

<400> 50

Met Glu Lys Ser Gly Ser Ala Asp Leu His Val Asn Ile Ile Glu Arg
1 5 10 15

Val Val Val Ala Pro Cys Gln Pro Thr Pro Lys Thr Ile Leu Gln Leu

20					25					30						
Ser	Ser	Ile	Asp	Lys	Met	Gly	Gly	Gly	Phe	Ala	Asn	Val	Leu	Leu	Val	
--35					40					45						
Phe	Gly	Ala	Ser	His	Gly	Val	Ser	Ala	Asp	Pro	Ala	Lys	Thr	Ile	Arg	
50					55					60						
Glu	Ala	Leu	Ser	Lys	Thr	Leu	Val	Phe	Tyr	Phe	Pro	Phe	Ala	Gly	Arg	
65					70					75					80	
Leu	Arg	Lys	Lys	Glu	Asp	Gly	Asp	Ile	Glu	Val	Glu	Cys	Ile	Glu	Gln	
85					90					95						
Gly	Ala	Leu	Phe	Val	Glu	Ala	Met	Ala	Asp	Asn	Asp	Leu	Ser	Val	Val	
100					105					110						
Arg	Asp	Leu	Asp	Glu	Tyr	Asn	Pro	Leu	Phe	Arg	Gln	Leu	Gln	Ser	Ser	
115					120					125						
Leu	Ser	Leu	Asp	Thr	Asp	Tyr	Lys	Asp	Leu	His	Leu	Met	Thr	Val	Gln	
130					135					140						
Val	Thr	Pro	Phe	Thr	Cys	Gly	Gly	Phe	Val	Met	Gly	Thr	Ser	Val	His	
145					150					155					160	
Gln	Ser	Ile	Cys	Asp	Gly	Asn	Gly	Leu	Gly	Gln	Phe	Phe	Lys	Ser	Met	
165					170					175						
Ala	Glu	Ile	Val	Arg	Gly	Glu	Val	Lys	Pro	Ser	Ile	Glu	Pro	Ile	Trp	
180					185					190						
Asn	Arg	Glu	Leu	Val	Lys	Pro	Glu	Asp	Tyr	Ile	His	Leu	Gln	Leu	Tyr	
195					200					205						
Val	Ser	Glu	Phe	Ile	Arg	Pro	Pro	Leu	Val	Val	Glu	Lys	Val	Gly	Gln	
210					215					220						
Thr	Ser	Leu	Val	Ile	Ser	Phe	Glu	Lys	Ile	Asn	His	Ile	Lys	Arg	Cys	
225					230					235					240	
Ile	Met	Glu	Glu	Ser	Lys	Glu	Ser	Phe	Ser	Ser	Phe	Glu	Ile	Val	Thr	
245					250					255						
Ala	Met	Val	Trp	Leu	Ala	Arg	Thr	Arg	Ala	Phe	Gln	Ile	Pro	His	Asn	
260					265					270						
Glu	Asp	Val	Thr	Leu	Leu	Leu	Ala	Met	Asp	Ala	Arg	Arg	Ser	Phe	Asp	
275					280					285						
Pro	Pro	Ile	Pro	Lys	Gly	Tyr	Tyr	Gly	Asn	Val	Ile	Gly	Thr	Thr	Tyr	
290					295					300						
Ala	Lys	Asp	Asn	Val	His	Asn	Leu	Leu	Ser	Gly	Ser	Leu	Leu	His	Ala	
305					310					315					320	
Leu	Thr	Val	Ile	Lys	Lys	Ser	Met	Ser	Ser	Phe	Tyr	Glu	Asn	Met	Thr	
325					330					335						
Ser	Arg	Val	Leu	Val	Asn	Pro	Ser	Thr	Leu	Asp	Leu	Ser	Met	Lys	Tyr	
340					345					350						

Glu Asn Val Val Ser Leu Ser Asp Trp Ser Arg Leu Gly His Asn Glu
 355 360 365

Val Asp Phe Gly Trp Gly Asn Ala Ile Asn Val Ser Thr Leu Gln Gln
 370 375 380

Gln Trp Glu Asn Glu Val Ala Ile Pro Thr Phe Phe Thr Phe Leu Gln
 385 390 395 400

Thr Pro Lys Asn Ile Pro Asp Gly Ile Lys Ile Leu Met Phe Met Pro
 405 410 415

Pro Ser Arg Glu Lys Thr Phe Glu Ile Glu Val Glu Ala Met Ile Arg
 420 425 430

Lys Tyr Leu Thr Lys Val Ser His Ser Lys Leu
 435 440

<210> 51
 <211> 1338
 <212> DNA
 <213> *Taxus cuspidata*

<400> 51
 atgaagaaga caggttcggt tgcagagttc catgtgaata tgattgagcg agtcatgggtg 60
 agaccgtgcc tgccttcgcc caaaacaatc ctccctctct ccgccattga caacatggca 120
 agagcttttt ctaacgtatt gctgggtctac gctgccaaaca tggacagagt ctctgcagat 180
 cctgcaaaag tgattcgaga ggctctctcc aagggtgctgg tttattatta cccttttgct 240
 gggcggtcca gaaataaaga aaatggggaa ctgaagtgg agtgcacagg gcagggtgtt 300
 ctgtttctgg aagccatggc tgacagcgac ctttcagtct taacagatct ggataactac 360
 aatccatcgt ttcagcaggt gattttttct ctaccacagg atacagatat tgaggacctc 420
 catctcttga ttgttcaggt aactcgtttt acatgtgggg gttttgttgt gggagcgaat 480
 gtgtatggta gtgcatgcga tgcaaaagga tttggccagt ttcttcaaag tatggcagag 540
 atggcgagag gagaggttaa gccctcgatt gaaccgatat ggaatagaga actggtgaag 600
 ctagaacatt gtatgccctt ccggatgagt catcttcaaa ttatacatgc acctgtaatt 660
 gaggagaaat ttgttcaaac atctcttggt ataaactttg agataataaa tcatatcaga 720
 cgacgcacatc tggaagaacg caaagaaagt ttatcttcat ttgaaattgt agcagcattg 780
 gtttggttag caaagataaa ggcttttcaa attccacata gtgagaatgt gaagcttctt 840
 tttgcaatgg acttgaggag atcattttaat cccctcttc cacatggata ctatggcaat 900
 gccttttggt tttgcatgtgc aatggataat gtccatgacc ttctaagtgg atctcttttg 960
 cgactataaa tgatcataaa gaaatcaaaag ttctctttac acaaagaact caactcaaaa 1020
 accgtgatga gctcatctgt agtagatgtc aatacgaagt ttgaagatgt agtttcaatt 1080
 agtgattgga ggcattctat atattatgaa gtggactttg ggtggggaga tgcaatgaac 1140
 gtgagcacta tgctacaaca acaggagcac gagaaatctc tgccaactta tttttctttc 1200
 ctacaatcta ctaagaacat gccagatgga atcaagatgc taatgtttat gcctccatca 1260
 aaactgaaaa aattcaaaat tgaaatagaa gctatgataa aaaaatatgt gactaaagtg 1320
 tgtccgtcaa agttatga 1338

<210> 52
 <211> 445
 <212> PRT
 <213> *Taxus cuspidata*

<400> 52
 Met Lys Lys Thr Gly Ser Phe Ala Glu Phe His Val Asn Met Ile Glu
 1 5 10 15

Arg Val Met Val Arg Pro Cys Leu Pro Ser Pro Lys Thr Ile Leu Pro
 20 25 30

Leu Ser Ala Ile Asp Asn Met Ala Arg Ala Phe Ser Asn Val Leu Leu
 35 40 45
 Val Tyr Ala Ala Asn Met Asp Arg Val Ser Ala Asp Pro Ala Lys Val
 50 55 60
 Ile Arg Glu Ala Leu Ser Lys Val Leu Val Tyr Tyr Tyr Pro Phe Ala
 65 70 75 80
 Gly Arg Leu Arg Asn Lys Glu Asn Gly Glu Leu Glu Val Glu Cys Thr
 85 90 95
 Gly Gln Gly Val Leu Phe Leu Glu Ala Met Ala Asp Ser Asp Leu Ser
 100 105 110
 Val Leu Thr Asp Leu Asp Asn Tyr Asn Pro Ser Phe Gln Gln Leu Ile
 115 120 125
 Phe Ser Leu Pro Gln Asp Thr Asp Ile Glu Asp Leu His Leu Leu Ile
 130 135 140
 Val Gln Val Thr Arg Phe Thr Cys Gly Gly Phe Val Val Gly Ala Asn
 145 150 155 160
 Val Tyr Gly Ser Ala Cys Asp Ala Lys Gly Phe Gly Gln Phe Leu Gln
 165 170 175
 Ser Met Ala Glu Met Ala Arg Gly Glu Val Lys Pro Ser Ile Glu Pro
 180 185 190
 Ile Trp Asn Arg Glu Leu Val Lys Leu Glu His Cys Met Pro Phe Arg
 195 200 205
 Met Ser His Leu Gln Ile Ile His Ala Pro Val Ile Glu Glu Lys Phe
 210 215 220
 Val Gln Thr Ser Leu Val Ile Asn Phe Glu Ile Ile Asn His Ile Arg
 225 230 235 240
 Arg Arg Ile Met Glu Glu Arg Lys Glu Ser Leu Ser Ser Phe Glu Ile
 245 250 255
 Val Ala Ala Leu Val Trp Leu Ala Lys Ile Lys Ala Phe Gln Ile Pro
 260 265 270
 His Ser Glu Asn Val Lys Leu Leu Phe Ala Met Asp Leu Arg Arg Ser
 275 280 285
 Phe Asn Pro Pro Leu Pro His Gly Tyr Tyr Gly Asn Ala Phe Gly Ile
 290 295 300
 Ala Cys Ala Met Asp Asn Val His Asp Leu Leu Ser Gly Ser Leu Leu
 305 310 315 320
 Arg Thr Ile Met Ile Ile Lys Lys Ser Lys Phe Ser Leu His Lys Glu
 325 330 335
 Leu Asn Ser Lys Thr Val Met Ser Ser Ser Val Val Asp Val Asn Thr
 340 345 350

Lys Phe Glu Asp Val Val Ser Ile Ser Asp Trp Arg His Ser Ile Tyr
 355 360 365
 Tyr Glu Val Asp Phe Gly Trp Gly Asp Ala Met Asn Val Ser Thr Met
 370 375 380
 Leu Gln Gln Gln Glu His Glu Lys Ser Leu Pro Thr Tyr Phe Ser Phe
 385 390 395 400
 Leu Gln Ser Thr Lys Asn Met Pro Asp Gly Ile Lys Met Leu Met Phe
 405 410 415
 Met Pro Pro Ser Lys Leu Lys Lys Phe Lys Ile Glu Ile Glu Ala Met
 420 425 430
 Ile Lys Lys Tyr Val Thr Lys Val Cys Pro Ser Lys Leu
 435 440 445

<210> 53
 <211> 1326
 <212> DNA
 <213> *Taxus cuspidata*

<400> 53
 atggagaagg caggctcaac agacttccat gtaaagaaat ttgatccagt catggtagcc 60
 ccaagccttc catcgcccaa agctaccgtc cagctctctg tcgttgatag cctaacaatc 120
 tgcaggggaa tttttaacac gttgttggtt ttcaatgccc ctgacaacat ttctgcagat 180
 cctgtaaaaa taattagaga ggctctctcc aagggtgttg tgtattattt ccctcttgct 240
 gggcggtcca gaagtaaaga aattggggaa cttgaagtgg agtgcacagg ggaatgggct 300
 ctgtttgtgg aagccatggt ggaagacacc atttcagtct tacgagatct ggatgacctc 360
 aatccatcat ttcagcagtt agtttttttg catccattgg acaactgctat tgaggatctt 420
 catcttgtga ttgttcaggt aacacgtttt acatgtgggg gcattgccgt tggagtgact 480
 ttgccccata gtgtatgtga tggacgtgga gcagcccagt ttgttacagc actggcagag 540
 atggcgaggg gagagggttaa gccctcacta gaaccaatat ggaatagaga attgttgaac 600
 cctgaagacc ctctacatct ccagttaaat caatttgatt cgatatgccc acctccaatg 660
 ctggaggaat tgggtcaagc ttcttttgtt ataaacgttg acaccataga atatatgaag 720
 caatgtgtca tggaggaatg taatgaattt tgttcgtctt ttgaagtagt ggcagcattg 780
 gtttgatag cacggacaaa ggctcttcaa attccacata ctgagaatgt gaagcttctc 840
 tttgcgatgg atttgaggaa attatttaac ccccaacttc caaatggata ttatggtaat 900
 gccattggta ctgcatatgc aatggataat gtccaagacc tcttaaatgg atctcttttg 960
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 ttgagtgact ggaggcgggt gggattttat gaagccgatt ttgggtgggg aggtccactg 1140
 aatgtaagtt ccctgcaacg gttggaaaat ggattgccta tgttttagtac ttttctatac 1200
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 gtgtga 1326

<210> 54
 <211> 441
 <212> PRT
 <213> *Taxus cuspidata*

<400> 54
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 Val Met Val Ala Pro Ser Leu Pro Ser Pro Lys Ala Thr Val Gln Leu
 20 25 30

Ser Val Val Asp Ser Leu Thr Ile Cys Arg Gly Ile Phe Asn Thr Leu
 35 40 45
 Leu Val Phe Asn Ala Pro Asp Asn Ile Ser Ala Asp Pro Val Lys Ile
 50 55 60
 Ile Arg Glu Ala Leu Ser Lys Val Leu Val Tyr Tyr Phe Pro Leu Ala
 65 70 75 80
 Gly Arg Leu Arg Ser Lys Glu Ile Gly Glu Leu Glu Val Glu Cys Thr
 85 90 95
 Gly Asp Gly Ala Leu Phe Val Glu Ala Met Val Glu Asp Thr Ile Ser
 100 105 110
 Val Leu Arg Asp Leu Asp Asp Leu Asn Pro Ser Phe Gln Gln Leu Val
 115 120 125
 Phe Trp His Pro Leu Asp Thr Ala Ile Glu Asp Leu His Leu Val Ile
 130 135 140
 Val Gln Val Thr Arg Phe Thr Cys Gly Gly Ile Ala Val Gly Val Thr
 145 150 155 160
 Leu Pro His Ser Val Cys Asp Gly Arg Gly Ala Ala Gln Phe Val Thr
 165 170 175
 Ala Leu Ala Glu Met Ala Arg Gly Glu Val Lys Pro Ser Leu Glu Pro
 180 185 190
 Ile Trp Asn Arg Glu Leu Leu Asn Pro Glu Asp Pro Leu His Leu Gln
 195 200 205
 Leu Asn Gln Phe Asp Ser Ile Cys Pro Pro Pro Met Leu Glu Glu Leu
 210 215 220
 Gly Gln Ala Ser Phe Val Ile Asn Val Asp Thr Ile Glu Tyr Met Lys
 225 230 235 240
 Gln Cys Val Met Glu Glu Cys Asn Glu Phe Cys Ser Ser Phe Glu Val
 245 250 255
 Val Ala Ala Leu Val Trp Ile Ala Arg Thr Lys Ala Leu Gln Ile Pro
 260 265 270
 His Thr Glu Asn Val Lys Leu Leu Phe Ala Met Asp Leu Arg Lys Leu
 275 280 285
 Phe Asn Pro Pro Leu Pro Asn Gly Tyr Tyr Gly Asn Ala Ile Gly Thr
 290 295 300
 Ala Tyr Ala Met Asp Asn Val Gln Asp Leu Leu Asn Gly Ser Leu Leu
 305 310 315 320
 Arg Ala Ile Met Ile Ile Lys Lys Ala Lys Ala Asp Leu Lys Asp Asn
 325 330 335
 Tyr Ser Arg Ser Arg Val Val Thr Asn Pro Tyr Ser Leu Asp Val Asn
 340 345 350
 Lys Lys Ser Asp Asn Ile Leu Ala Leu Ser Asp Trp Arg Arg Leu Gly

355

360

365

Phe Tyr Glu Ala Asp Phe Gly Trp Gly Gly Pro Leu Asn Val Ser Ser
370 -- 375 380

Leu Gln Arg Leu Glu Asn Gly Leu Pro Met Phe Ser Thr Phe Leu Tyr
385 390 395 400

Leu Leu Pro Ala Lys Asn Lys Ser Asp Gly Ile Lys Leu Leu Leu Ser
405 410 415

Cys Met Pro Pro Thr Thr Leu Lys Ser Phe Lys Ile Val Met Glu Ala
420 425 430

Met Ile Glu Lys Tyr Val Ser Lys Val
435 440

<210> 55

<211> 1347

<212> DNA

<213> *Taxus cuspidata*

<400> 55

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gacagactgc cagggatgaa gtttgctact tttagcgccg tgttagtcta caatgccagc 180
tctcaactcca tttttgcaaa tcctgcacag attattcggc aggcctctctc caaggtgttg 240
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gctatgcgaa attattttct tttccttcga ccttacaagg acatgcctaa tggaatcaaa 1260
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ataattaaat atatgccgaa agcctaa 1347

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<210> 56

<211> 448

<212> PRT

<213> *Taxus cuspidata*

<400> 56

Met Glu Lys Gly Asn Ala Ser Asp Val Pro Glu Leu His Val Gln Ile
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Cys Glu Arg Val Met Val Lys Pro Cys Val Pro Ser Pro Ser Pro Asn
20 25 30

Leu Val Leu Gln Leu Ser Ala Val Asp Arg Leu Pro Gly Met Lys Phe

35

40

45

Ala Thr Phe Ser Ala Val Leu Val Tyr Asn Ala Ser Ser His Ser Ile
 50 -- 55 60
 Phe Ala Asn Pro Ala Gln Ile Ile Arg Gln Ala Leu Ser Lys Val Leu
 65 70 75 80
 Gln Tyr Tyr Pro Ala Phe Ala Gly Arg Ile Arg Gln Lys Glu Asn Glu
 85 90 95
 Glu Leu Glu Val Glu Cys Thr Gly Glu Gly Ala Leu Phe Val Glu Ala
 100 105 110
 Leu Val Asp Asn Asp Leu Ser Val Leu Arg Asp Leu Asp Ala Gln Asn
 115 120 125
 Ala Ser Tyr Glu Gln Leu Leu Phe Ser Leu Pro Pro Asn Ile Gln Val
 130 135 140
 Gln Asp Leu His Pro Leu Ile Leu Gln Val Thr Arg Phe Thr Cys Gly
 145 150 155 160
 Gly Phe Val Val Gly Val Gly Phe His His Gly Ile Cys Asp Ala Arg
 165 170 175
 Gly Gly Thr Gln Phe Leu Gln Gly Leu Ala Asp Met Ala Arg Gly Glu
 180 185 190
 Thr Lys Pro Leu Val Glu Pro Val Trp Asn Arg Glu Leu Ile Lys Pro
 195 200 205
 Glu Asp Leu Met His Leu Gln Phe His Lys Phe Gly Leu Ile Arg Gln
 210 215 220
 Pro Leu Lys Leu Asp Glu Ile Cys Gln Ala Ser Phe Thr Ile Asn Ser
 225 230 235 240
 Glu Ile Ile Asn Tyr Ile Lys Gln Cys Val Ile Glu Glu Cys Asn Glu
 245 250 255
 Ile Phe Ser Ala Phe Glu Val Val Val Ala Leu Thr Trp Ile Ala Arg
 260 265 270
 Thr Lys Ala Phe Gln Ile Pro His Asn Glu Asn Val Met Met Leu Phe
 275 280 285
 Gly Met Asp Ala Arg Lys Tyr Phe Asn Pro Pro Leu Pro Lys Gly Tyr
 290 295 300
 Tyr Gly Asn Ala Ile Gly Thr Ser Cys Val Ile Glu Asn Val Gln Asp
 305 310 315 320
 Leu Leu Asn Gly Ser Leu Ser Arg Ala Val Met Ile Thr Lys Lys Ser
 325 330 335
 Lys Ile Pro Leu Ile Glu Asn Leu Arg Ser Arg Ile Val Ala Asn Gln
 340 345 350
 Ser Gly Val Asp Glu Glu Ile Lys His Glu Asn Val Val Gly Phe Gly
 355 360 365

Asp Trp Arg Arg Leu Gly Phe His Glu Val Asp Phe Gly Ser Gly Asp
 370 375 380

Ala Val Asn Ile Ser Pro Ile Gln Gln Arg Leu Glu Asp Asp Gln Leu
 385 390 395 400

Ala Met Arg Asn Tyr Phe Leu Phe Leu Arg Pro Tyr Lys Asp Met Pro
 405 410 415

Asn Gly Ile Lys Ile Leu Met Phe Met Asp Pro Ser Arg Val Lys Leu
 420 425 430

Phe Lys Asp Glu Met Glu Ala Met Ile Ile Lys Tyr Met Pro Lys Ala
 435 440 445

<210> 57
 <211> 1317
 <212> DNA
 <213> *Taxus cuspidata*

<400> 57
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 ttgttcgtct acgacagggt ttcaactgtt tctgcaaatac ctgcaaaaac aattcgagag 180
 gctctctcca aggttttggg ttattattca ccttttgctg gaaggctcag aaacaaagaa 240
 aatggggatc ttgaagtgga gtgcagtggg gaggtgctg tctttgtgga agccatggcg 300
 gacaacgagc tttcagtcctt acaagatttg gatgagtact gtacatcgct taaacagcta 360
 atttttacag taccaatgga tacgaaaatt gaagacctcc atcttctaag tggttcaggta 420
 actagtttta catgtggggg atttgtttgt ggaataagtt tctaccatac tatatgtgat 480
 ggaaaaggac tgggccagtt tcttcaaggc atgagtgaga tttccaaggg agcattttaa 540
 ccctcactag aaccagtatg gaatagagaa atggtgaagc ctgaacacct tatgttcctc 600
 cagtttaata attttgaatt cgtaccacat cctcttaaat ttaagaagat tgttaaagca 660
 tctattgaaa ttaactttga gacaataaat tgtttcaagc aatgcatgat ggaagaatgt 720
 aaagaaaatt tctctacatt tgaaattgta gcagcactga tttggctagc caagacaaag 780
 tctttccaaa ttccagatag tgagaatgtg aaacttatgt ttgcagtoga catgaggaca 840
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 aagacaattt tctcttttaa agataatttc atatcaagaa gattgatgaa accatctaca 1020
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 tattatgagg cagattgtgg gtgtggaaat ctatcaaata taattcccat ggatcaacaa 1140
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 caaaatggaa tcaagatact aatgtccatg cctgaatcaa tggcgaaacc attcaaaagt 1260
 gaaatgaaat tcacaataaa aaaatatgtg actggagcgt gtttctctga gttatga 1317

<210> 58
 <211> 438
 <212> PRT
 <213> *Taxus cuspidata*

<400> 58
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Cys Leu Pro Ser Ser Lys Glu Ile Leu Gln Leu Ser Ser Leu Asp Asn
 20 25 30

Ile Leu Arg Cys Tyr Val Ser Val Leu Phe Val Tyr Asp Arg Val Ser
 35 40 45
 Thr Val Ser Ala Asn Pro Ala Lys Thr Ile Arg Glu Ala Leu Ser Lys
 50 55 60
 Val Leu Val Tyr Tyr Ser Pro Phe Ala Gly Arg Leu Arg Asn Lys Glu
 65 70 75 80
 Asn Gly Asp Leu Glu Val Glu Cys Ser Gly Glu Gly Ala Val Phe Val
 85 90 95
 Glu Ala Met Ala Asp Asn Glu Leu Ser Val Leu Gln Asp Leu Asp Glu
 100 105 110
 Tyr Cys Thr Ser Leu Lys Gln Leu Ile Phe Thr Val Pro Met Asp Thr
 115 120 125
 Lys Ile Glu Asp Leu His Leu Leu Ser Val Gln Val Thr Ser Phe Thr
 130 135 140
 Cys Gly Gly Phe Val Val Gly Ile Ser Phe Tyr His Thr Ile Cys Asp
 145 150 155 160
 Gly Lys Gly Leu Gly Gln Phe Leu Gln Gly Met Ser Glu Ile Ser Lys
 165 170 175
 Gly Ala Phe Lys Pro Ser Leu Glu Pro Val Trp Asn Arg Glu Met Val
 180 185 190
 Lys Pro Glu His Leu Met Phe Leu Gln Phe Asn Asn Phe Glu Phe Val
 195 200 205
 Pro His Pro Leu Lys Phe Lys Lys Ile Val Lys Ala Ser Ile Glu Ile
 210 215 220
 Asn Phe Glu Thr Ile Asn Cys Phe Lys Gln Cys Met Met Glu Glu Cys
 225 230 235 240
 Lys Glu Asn Phe Ser Thr Phe Glu Ile Val Ala Ala Leu Ile Trp Leu
 245 250 255
 Ala Lys Thr Lys Ser Phe Gln Ile Pro Asp Ser Glu Asn Val Lys Leu
 260 265 270
 Met Phe Ala Val Asp Met Arg Thr Ser Phe Asp Pro Pro Leu Pro Lys
 275 280 285
 Gly Tyr Tyr Gly Asn Val Ile Gly Ile Ala Gly Ala Ile Asp Asn Val
 290 295 300
 Lys Glu Leu Leu Ser Gly Ser Ile Leu Arg Ala Leu Ile Ile Ile Gln
 305 310 315 320
 Lys Thr Ile Phe Ser Leu Lys Asp Asn Phe Ile Ser Arg Arg Leu Met
 325 330 335
 Lys Pro Ser Thr Leu Asp Val Asn Met Lys His Glu Asn Val Val Leu
 340 345 350
 Leu Gly Asp Trp Arg Asn Leu Gly Tyr Tyr Glu Ala Asp Cys Gly Cys

355		360		365											
Gly	Asn	Leu	Ser	Asn	Val	Ile	Pro	Met	Asp	Gln	Gln	Ile	Glu	His	Glu
370	--					375					380				
Ser	Pro	Val	Gln	Ser	Arg	Phe	Met	Leu	Leu	Arg	Ser	Ser	Lys	Asn	Met
385					390					395					400
Gln	Asn	Gly	Ile	Lys	Ile	Leu	Met	Ser	Met	Pro	Glu	Ser	Met	Ala	Lys
				405					410					415	
Pro	Phe	Lys	Ser	Glu	Met	Lys	Phe	Thr	Ile	Lys	Lys	Tyr	Val	Thr	Gly
			420					425					430		
Ala	Cys	Phe	Ser	Glu	Leu										
	435														